

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1-20. (Cancelled).

21. (Currently Amended) A method for assessing the affect of a treatment on a population of cells ~~cell~~, comprising:

exposing a population of cells to the treatment;

capturing an image of a plurality of cells from the population;

automatically obtaining a plurality of first cellular features from the image,

wherein the first cellular features are characteristic of a nuclear morphology property of the cells in the population;

automatically obtaining a plurality of second cellular features from the image,

wherein the second cellular features are characteristic of an inter-nuclear property of the cells in the population;

automatically analyzing the plurality of first cellular features and the plurality of second cellular features to automatically ~~determining~~ determine the abundance of bi-nuclear cells in the population; and

automatically classifying the treatment based on the distribution of the nuclear morphology property, distribution of the inter-nuclear property, and abundance of bi-nuclear cells in the population;

wherein the automatic classifying comprises comparing the distribution of the nuclear morphology property, distribution of the inter-nuclear property, and abundance of bi-nuclear cells in the population to a database of similar data derived from control untreated cells or cells subjected to a plurality of treatments; and

wherein the treatment is classified in terms of its affect on cytokinesis.

22-25. (Cancelled).

26. (Currently Amended) A method for characterising cells, comprising:
automatically determining, from a captured image of a nuclear component of a plurality of cells, the number of concave portions in the outline of the image of the nuclear component, wherein a concave portion in the outline of the image of the nuclear component is identified by automatically determining the angle subtended by adjacent portions of the outline, wherein identifying a concave portion further includes determining whether the angle is less than a threshold angle; and

automatically characterising the cell based on the number of concave portions;
wherein at least one determined characteristic of the cells is outputted to at least one of a display and a memory device.

27-33. (Cancelled).

34. (Currently Amended) A method for characterising cells, comprising:

automatically determining, from a captured image of a nuclear component of a plurality of cells, the number of concave portions in the outline of the image of the nuclear component; and

automatically characterising the cell based on the number of concave portions;

wherein characterising the cell further includes assessing a further feature of a nuclear image of the nuclear component;

wherein the further feature of the image of the nuclear component is the total intensity of the image of the nuclear component;

wherein the cell is automatically characterised as multinucleate if there are two or more concave portions and the total intensity exceeds a first threshold; and

wherein the cell is automatically characterized as bi-nuclear if the cell is not characterised as multi-nuclear and has more than one concave portion and the total intensity exceeds a second threshold which is less than the first threshold;

wherein at least one determined characteristic of the cells is outputted to at least one of a display and a memory device.

35-38. (Cancelled).

39. (Currently Amended) A method of identifying bi-nuclear cells, comprising:

automatically identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;

automatically determining, from a captured image of a cytoplasmic component of the plurality of cells, a measure of the amount of the cytoplasmic component interposed between the pair of nuclear components; and

automatically characterising the cells based on the measure of the amount of the cytoplasmic component, wherein the measure is the detected intensity of the image of the cytoplasmic component;

wherein automatically determining a measure of the amount of the cytoplasmic component interposed between the pair of nuclear components is by a method comprising:

automatically identifying a straight path between the pair of nuclear components;
and

automatically determining the amount of the cytoplasmic component that falls under the path;

wherein at least one determined characteristic of the cells is outputted to at least one of a display and a memory device.

40. (Original) The method as claimed in claim 39, wherein the path extends between the centroids of the pair of nuclear components.

41. (Previously Presented) The method as claimed in claim 40, wherein the amount of cytoplasmic component is automatically determined by summing over the path extending between the peripheries of the nuclear components.

42-50. (Cancelled).

51. (Currently Amended) A method for automatically identifying biologically relevant pairs of nuclei, comprising:

automatically identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;

automatically identifying, from the captured image, a nearest neighbour nuclear component to the pair of nuclear components; and

automatically characterising the cells associated with the pair of nuclear components based on the separation of the pair of nuclear components and the separation of the next nearest neighbour nuclear component from the pair of nuclear components;

wherein automatically characterising the cell includes determining if the separation of the pair of nuclear components is less than a first threshold and the separation of the next nearest neighbour nuclear component and pair of nuclear components is greater than a second threshold;

wherein at least one determined characteristic of the cells is outputted to at least one of a display and a memory device.

52. (Original) The method as claimed in claim 51, wherein the second threshold is at least twice the first threshold.

53. (Original) The method as claimed in claim 51, wherein the separation between the pair of nuclear components is the shortest distance between the outlines of the nuclear components.

55. (Previously Presented) The method as claimed in claim 54, wherein automatically identifying the set of candidate nuclear components includes determining the separation between the centroids of the nuclear components for each of the candidate pairs.

56. (Original) The method as claimed in claim 51 wherein the first and second thresholds are computed based on the density of nuclear components in the captured image.

57. (Previously Presented) The method as claimed in claim 51, wherein the cell associated with the pair of nuclear components is automatically characterised as bi-nuclear if the separation of the pair of nuclear components is automatically determined to be less than the first threshold and the separation of the next nearest neighbour nuclear component and pair of nuclear components is automatically determined to be greater than the second threshold.

58. (Previously Presented) The method as claimed in claim 57, further comprising automatically determining the proportion of bi-nuclear cells in the captured image.

59. (Currently Amended) A computer program product comprising a machine readable medium on which is provided program instructions for identifying biologically relevant pairs of nuclei, the instructions comprising:

(a) code for automatically identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;

(b) code for automatically identifying, from the captured image, a nearest neighbour nuclear component to the pair of nuclear components; and

(c) code for automatically characterising the cell associated with the pair of nuclear components based on the separation of the pair of nuclear components and the separation of the next nearest neighbour nuclear component from the pair of nuclear components;

wherein at least one determined characteristic of the cells is outputted to at least one of a display and a memory device.

60. (Currently Amended) A computing device comprising a memory device configured to store at least temporarily program instructions for automatically identifying biologically relevant pairs of nuclei , the instructions comprising:

code for automatically identifying, from a captured image of a nuclear component of a plurality of cells, at least one pair of nuclear components;

code for automatically identifying, from the captured image, a nearest neighbour nuclear component to the pair of nuclear components; and

code for automatically characterising the cell associated with the pair of nuclear components based on the separation of the pair of nuclear components and the separation of the next nearest neighbour nuclear component from the pair of nuclear components;

wherein at least one determined characteristic of the cells is outputted to at least one of a display and a memory device.

61. (Currently Amended) A method as claimed in claim 21, wherein the plurality of first cellular features includes nuclear features.

62. (Currently Amended) A method as claimed in claim 21, wherein the plurality of second cellular features ~~further~~ includes cytoplasmic features.

63. (Previously Presented) The method as claimed in claim 26, further comprising smoothing the outline of the image of the nuclear component.

64. (Previously Presented) The method as claimed in claim 63, wherein smoothing the outline of the image of the nuclear component includes converting the outline into a polygon.

65. (Previously Presented) The method as claimed in claim 26, wherein the cell is automatically characterised based on the number of concave portions identified and a secondary criterion

66. (Previously Presented) The method as claimed in claim 65, wherein the secondary criterion is indicative of the amount of nuclear material.

67. (Previously Presented) The method as claimed in claim 26, wherein the cell is characterised as multi-nuclear if more than two concave portions are identified.

68. (Previously Presented) The method as claimed in claim 26, wherein characterising the cell further includes assessing a further feature of a nuclear image of the nuclear component

69. (Previously Presented) The method as claimed in claim 68, wherein the further feature of the image of the nuclear component is the total intensity of the image of the nuclear component.

70. (Previously Presented) The method as claimed in claim 69, wherein the cell is automatically characterised as multinucleate if there are two or more concave portions and the total intensity exceeds a first threshold.

71. (Previously Presented) The method as claimed in claim 39, further including automatically removing particular nuclear components from the image prior to identifying pairs.

72. (Previously Presented) The method as claimed in claim 71, wherein the particular nuclear components are selected from nuclear components of mitotic cells; nuclear components at the edge of the image; multinucleate nuclear components; nuclear components having an image intensity exceeding a threshold; and nuclear components having an image intensity below a threshold.

73. (Previously Presented) The method as claimed in claim 39, wherein characterising the cells further includes automatically comparing the measure of the amount of the cytoplasmic component with a measure of the amount of the same cytoplasmic component for a control group of cells.

74. (Previously Presented) The method as claimed in claim 73, wherein the measure of the amount for the control group corresponds to the proportion of bi-nuclear cells expected in the control group.

75. (Previously Presented) The method as claimed in claim 74, wherein the proportion of bi-nuclear cells expected in the control group is not more than 4%.